SEQUENCE LISTING

- <110> ROSENBLUM, MICHAEL G. CHEUNG, LAWRENCE
- <120> MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF MAKING THEEOF
- <130> CLFR:007US
- <140> UNKNOWN
- <141> 2002-02-12
- <150> 60/268,402
- <151> 2001-02-12
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- Asp Thr Val Ser Phe Ser Thr Lys Gly Ala Thr Tyr Ile Thr Tyr Val 50 55 60
- Asn Phe Leu Asn Glu Leu Arg Val Lys Leu Lys Pro Glu Gly Asn Ser 65 70 75 80
- His Gly Ile Pro Leu Leu Arg Lys Lys Cys Asp Asp Pro Gly Lys Cys 85 90 95
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- Ala Ile Asp Val Thr Ser Val Tyr Val Val Gly Tyr Gln Val Arg Asn 115 120 125
- Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu Gly Leu 130 135 140
- Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser Tyr Pro 145 150 155 160
- Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu Gly Ile

165

THE REAL PROPERTY OF MINISTERS AND ASSESSED.

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Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala Ile Asp 190 185 180

Asn Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val Ile Gln 205 200 195

Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln Ile Arg 220 215 210

Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile Ser Leu 235 230

Glu Asn Lys Trp Gly Lys Leu Ser Phe Gln Ile Arg Thr Ser Gly Ala 250 245

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Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile Ala Leu 285 280 275

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aag Lys 305	Cys	ttc Phe	gtt Val	ttg Leu	gta Val 310	. Ala	ctt Leu	tca Ser	. aat Asn	gac Asp 315	Asn	gga Gly	cag Gln	ttg Lev	gcg Ala 320	960
gaa Glu	ata Ile	gct Alæ	ata Ile	gat Asp	gtt Val	aca Thr	agt Ser	gtt Val	tat Tyr	gtg Val	gtg Val	ggc Gly	tat Tyr	caa Glr	gta Val	1008

335 330 325

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Tyr	ccc Pro 370	tcg Ser	ctg Leu	gaa Glu	ggt Gly	gag Glu 375	aag Lys	gca Ala	tat Tyr	aga Arg	gag Glu 380	aca Thr	aca Thr	gac Asp	ttg Leu	1152
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Leu Leu Phe Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe 50 55 60

Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val 65 70 75 80

Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr 85 90 95

Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr 100 105 110

Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu 115 120 125

Val Lys Val Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser 130 135 140

Met Lys Leu Ser Cys Val Val Ser Gly Phe Thr Phe Gly Asn Tyr Trp 145 150 155 160

Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Ala 165 170 175

Glu Ile Arg Leu Lys Ser Asn Asn Phe Ala Arg Tyr Tyr Ala Glu Ser 180 185 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser Val 195 200 205

Tyr Leu Gln Met Ile Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr Tyr 210 215 220

Cys Thr Ser Tyr Gly Asn Tyr Val Gly His Tyr Phe Asp His Trp Gly 235 230 240

Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Gly Gly Gly Ser 245 250 255

Gly Leu Asp Thr Val Ser Phe Ser Thr Lys Gly Ala Thr Tyr Ile Thr 260 265 270

Tyr Val Asn Phe Leu Asn Glu Leu Arg Val Lys Leu Lys Pro Glu Gly 275 280 285

Asn Ser His Gly Ile Pro Leu Leu Arg Lys Lys Cys Asp Asp Pro Gly 290 295 300

Lys Cys Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala 305 310 315 320

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- Gly Leu Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser 355 360 365
- Tyr Pro Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu 370 380
- Gly Ile Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala 385 390 395 400
- Ile Asp Asn Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val 405 410 415
- Ile Gln Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln 420 425 430
- Ile Arg Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile 435 440 445
- Ser Leu Glu Asn Lys Trp Gly Lys Leu Ser Phe Gln Ile Arg Thr Ser 450 455 460
- Gly Ala Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn 465 470 475 480
- Gly Lys Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile 485 490 495
- Ala Leu Leu Lys Phe Val Asp Lys Asp Pro Lys 500 505